

SEQUENCE LISTING

<110> Abrahmsén , Lars
Nilsson, Joakim

<120> METHODS FOR PROTEIN PURIFICATION

<130> 13425-053001

<150> SE 0100625-3

<151> 2001-02-23

<150> US 60/272,247

<151> 2001-02-28

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4040

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (161)...(2449)

<400> 1

```

gtccttccca cccttagtcc caggcattctg actaccggga acctcagcca gagtccggga      60
gccccccacc cgtccagga gccaacagag cccccgtctt gctggcgtga gaatacattg      120
ctctcctttg gttgaatcag ctgtccctct tegtgggaaa atg aac cag aag aca      175
                                   Met Asn Gln Lys Thr
                                   1           5

atc ctc gtg ctc ctc att ctg gcc gtc atc acc atc ttt gcc ttg gtt      223
Ile Leu Val Leu Leu Ile Leu Ala Val Ile Thr Ile Phe Ala Leu Val
              10              15              20

tgt gtc ctg ctg gtg ggc agg ggt gga gat ggg ggt gaa ccc agc cag      271
Cys Val Leu Leu Val Gly Arg Gly Gly Asp Gly Gly Glu Pro Ser Gln
              25              30              35

ctt ccc cat tgc ccc tct gta tct ccc agt gcc cag cct tgg aca cac      319
Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala Gln Pro Trp Thr His
              40              45              50

cct ggc cag agc cag ctg ttt gca gac ctg agc cga gag gag ctg acg      367
Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser Arg Glu Glu Leu Thr
              55              60              65

gct gtg atg cgc ttt ctg acc cag cgg ctg ggg cca ggg ctg gtg gat      415
Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly Pro Gly Leu Val Asp
              70              75              80              85

```

13425-053001

gca gcc cag gcc cgg ccc tcg gac aac tgt gtc ttc tca gtg gag ttg	463
Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val Phe Ser Val Glu Leu	
90 95 100	
cag ctg cct ccc aag gct gca gcc ctg gct cac ttg gac agg ggg agc	511
Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His Leu Asp Arg Gly Ser	
105 110 115	
ccc cca cct gcc cgg gag gca ctg gcc atc gtc ttc ttt ggc agg caa	559
Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val Phe Phe Gly Arg Gln	
120 125 130	
ccc cag ccc aac gtg agt gag ctg gtg gtg ggg cca ctg cct cac ccc	607
Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly Pro Leu Pro His Pro	
135 140 145	
tcc tac atg cgg gac gtg act gtg gag cgt cat gga ggc ccc ctg ccc	655
Ser Tyr Met Arg Asp Val Thr Val Glu Arg His Gly Gly Pro Leu Pro	
150 155 160 165	
tat cac cga cgc ccc gtg ctg ttc caa gag tac ctg gac ata gac cag	703
Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr Leu Asp Ile Asp Gln	
170 175 180	
atg atc ttc aac aga gag ctg ccc cag gct tct ggg ctt ctc cac cac	751
Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser Gly Leu His His	
185 190 195	
tgt tgc ttc tac aag cac cgg gga cgg aac ctg gtg aca atg acc acg	799
Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu Val Thr Met Thr Thr	
200 205 210	
gct ccc cgt ggt ctg caa tca ggg gac cgg gcc acc tgg ttt ggc ctc	847
Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala Thr Trp Phe Gly Leu	
215 220 225	
tac tac aac atc tcg ggc gct ggg ttc ttc ctg cac cac gtg ggc ttg	895
Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu His His Val Gly Leu	
230 235 240 245	
gag ctg cta gtg aac cac aag gcc ctt gac cct gcc cgc tgg act atc	943
Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro Ala Arg Trp Thr Ile	
250 255 260	
cag aag gtg ttc tat caa ggc cgc tac tac gac agc ctg gcc cag ctg	991
Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp Ser Leu Ala Gln Leu	
265 270 275	
gag gcc cag ttt gag gcc ggc ctg gtg aat gtg gtg ctg atc cca gac	1039
Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val Val Leu Ile Pro Asp	
280 285 290	
aat ggc aca ggt ggg tcc tgg tcc ctg aag tcc cct gtg ccc ccg ggt	1087
Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser Pro Val Pro Pro Gly	
295 300 305	
cca gct ccc cct cta cag ttc tat ccc caa ggc ccc cgc ttc agt gtc	1135

Pro	Ala	Pro	Pro	Leu	Gln	Phe	Tyr	Pro	Gln	Gly	Pro	Arg	Phe	Ser	Val	
310					315					320					325	
cag	gga	agt	cga	gtg	gcc	tcc	tca	ctg	tgg	act	ttc	tcc	ttt	ggc	ctc	1183
Gln	Gly	Ser	Arg	Val	Ala	Ser	Ser	Leu	Trp	Thr	Phe	Ser	Phe	Gly	Leu	
				330					335					340		
gga	gca	ttc	agt	ggc	cca	agg	atc	ttt	gac	gtt	cgc	ttc	caa	gga	gaa	1231
Gly	Ala	Phe	Ser	Gly	Pro	Arg	Ile	Phe	Asp	Val	Arg	Phe	Gln	Gly	Glu	
			345					350					355			
aga	cta	gtt	tat	gag	ata	agc	ctc	caa	gag	gcc	ttg	gcc	atc	tat	ggt	1279
Arg	Leu	Val	Tyr	Glu	Ile	Ser	Leu	Gln	Glu	Ala	Leu	Ala	Ile	Tyr	Gly	
		360					365					370				
gga	aat	tcc	cca	gca	gca	atg	acg	acc	cgc	tat	gtg	gat	gga	ggc	ttt	1327
Gly	Asn	Ser	Pro	Ala	Ala	Met	Thr	Thr	Arg	Tyr	Val	Asp	Gly	Gly	Phe	
	375					380				385						
ggc	atg	ggc	aag	tac	acc	acg	ccc	ctg	acc	cgt	ggg	gtg	gac	tgc	ccc	1375
Gly	Met	Gly	Lys	Tyr	Thr	Thr	Pro	Leu	Thr	Arg	Gly	Val	Asp	Cys	Pro	
390					395					400				405		
tac	ttg	gcc	acc	tac	gtg	gac	tgg	cac	ttc	ctt	ttg	gag	tcc	cag	gcc	1423
Tyr	Leu	Ala	Thr	Tyr	Val	Asp	Trp	His	Phe	Leu	Leu	Glu	Ser	Gln	Ala	
				410					415					420		
ccc	aag	aca	ata	cgt	gat	gcc	ttt	tgt	gtg	ttt	gaa	cag	aac	cag	ggc	1471
Pro	Lys	Thr	Ile	Arg	Asp	Ala	Phe	Cys	Val	Phe	Glu	Gln	Asn	Gln	Gly	
			425					430					435			
ctc	ccc	ctg	cgg	cga	cac	cac	tca	gat	ctc	tac	tcg	cac	tac	ttt	ggg	1519
Leu	Pro	Leu	Arg	Arg	His	His	Ser	Asp	Leu	Tyr	Ser	His	Tyr	Phe	Gly	
		440					445					450				
ggt	ctt	gcg	gaa	acg	gtg	ctg	gtc	gtc	aga	tct	atg	tcc	acc	ttg	ctc	1567
Gly	Leu	Ala	Glu	Thr	Val	Leu	Val	Val	Arg	Ser	Met	Ser	Thr	Leu	Leu	
	455					460				465						
aac	tat	gac	tat	gtg	tgg	gat	acg	gtc	ttc	cac	ccc	agt	ggg	gcc	ata	1615
Asn	Tyr	Asp	Tyr	Val	Trp	Asp	Thr	Val	Phe	His	Pro	Ser	Gly	Ala	Ile	
470					475				480					485		
gaa	ata	cga	ttc	tat	gcc	acg	ggc	tac	atc	agc	tcg	gca	ttc	ctc	ttt	1663
Glu	Ile	Arg	Phe	Tyr	Ala	Thr	Gly	Tyr	Ile	Ser	Ser	Ala	Phe	Leu	Phe	
				490					495					500		
ggt	gct	act	ggg	aag	tac	ggg	aac	caa	gtg	tca	gag	cac	acc	ctg	ggc	1711
Gly	Ala	Thr	Gly	Lys	Tyr	Gly	Asn	Gln	Val	Ser	Glu	His	Thr	Leu	Gly	
			505					510					515			
acg	gtc	cac	acc	cac	agc	gcc	cac	ttc	aag	gtg	gat	ctg	gat	gta	gca	1759
Thr	Val	His	Thr	His	Ser	Ala	His	Phe	Lys	Val	Asp	Leu	Asp	Val	Ala	
		520					525					530				
gga	ctg	gag	aac	tgg	gtc	tgg	gcc	gag	gat	atg	gtc	ttt	gtc	ccc	atg	1807
Gly	Leu	Glu	Asn	Trp	Val	Trp	Ala	Glu	Asp	Met	Val	Phe	Val	Pro	Met	

1183
 1231
 1279
 1327
 1375
 1423
 1471
 1519
 1567
 1615
 1663
 1711
 1759
 1807

535	540	545	
gct gtg ccc tgg agc cct gag cac cag ctg cag agg ctg cag gtg acc			1855
Ala Val Pro Trp Ser	Pro Glu His Gln Leu	Gln Arg Leu Gln Val Thr	
550	555	560	565
cgg aag ctg ctg gag atg gag gag cag gcc gcc ttc ctc gtg gga agc			1903
Arg Lys Leu Leu	Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser		
	570	575	580
gcc acc cct cgc tac ctg tac ctg gcc agc aac cac agc aac aag tgg			1951
Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp			
	585	590	595
ggt cac ccc cgg ggc tac cgc atc cag atg ctc agc ttt gct gga gag			1999
Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu			
	600	605	610
ccg ctg ccc caa aac agc tcc atg gcg aga ggc ttc agc tgg gag agg			2047
Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg			
	615	620	625
tac cag ctg gct gtg acc cag cgg aag gag gag gag ccc agt agc agc			2095
Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser			
	630	635	640
agc gtt ttc aat cag aat gac cct tgg gcc ccc act gtg gat ttc agt			2143
Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro Thr Val Asp Phe Ser			
	650	655	660
gac ttc atc aac aat gag acc att gct gga aag gat ttg gtg gcc tgg			2191
Asp Phe Ile Asn Asn Glu Thr Ile Ala Gly Lys Asp Leu Val Ala Trp			
	665	670	675
gtg aca gct ggt ttt ctg cat atc cca cat gca gag gac att cct aac			2239
Val Thr Ala Gly Phe Leu His Ile Pro His Ala Glu Asp Ile Pro Asn			
	680	685	690
aca gtg act gtg ggg aac ggc gtg ggc ttc ttc ctc cga ccc tat aac			2287
Thr Val Thr Val Gly Asn Gly Val Gly Phe Phe Leu Arg Pro Tyr Asn			
	695	700	705
ttc ttt gac gaa gac ccc tcc ttc tac tct gcc gac tcc atc tac ttc			2335
Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala Asp Ser Ile Tyr Phe			
	710	715	720
cga ggg gac cag gat gct ggg gcc tgc gag gtc aac ccc cta gct tgc			2383
Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val Asn Pro Leu Ala Cys			
	730	735	740
ctg ccc cag gct gct gcc tgt gcc ccc gac ctc cct gcc ttc tcc cac			2431
Leu Pro Gln Ala Ala Ala Cys Ala Pro Asp Leu Pro Ala Phe Ser His			
	745	750	755
ggg ggc ttc tct cac aac taggcgggtcc tgggatgggg catgtggcca			2479
Gly Gly Phe Ser His Asn			
	760		

agggctccag ggccaggggtg tgagggatgg ggagcagctg ggcactgggc cggcagcctg 2539
 gtccctctt tcctgtgcca ggactctctt tcttccacta ccctccctcg catccgcctc 2599
 tgagccagga gcctcctgac cctgtgatgc ctgacacagg ggacactgaa ccttggtgat 2659
 gccagctgta ctgagttctc atccacagag gccaggcatg gccagcctg gagccgtggc 2719
 cgagggcttc cctagatggg tccctttgtt gctgtctggc tttcccgaa ctttttaggc 2779
 cacctccaag gactctaaaa gggggctatt ccttgagac cccagagtag ggttgccagt 2839
 cctgcaagtc catagctgag ctggaaagga tgcttctgct cacattccct ctcattccagg 2899
 tcccttccct ctgctcttcc tctctctcac ctacttctc ctcctcctcc tgttccctgcc 2959
 ttctcttcta tcctgcaatt tctcccgaa cctgagggga tatccctatg tcccagcccc 3019
 tggtaactccc ccagccctca gttttcagtc aagttccgtc tcctctccag ccctatggaa 3079
 gtctcaaggc cacgggaccc ctaatcagag tggccaatcc ctgtgtgtcg ttcccttggtg 3139
 tctgttgctt attgggagta ggagttgctc ctacccctgt cctggggctg ggtgtgtttc 3199
 aggacagctg cttctgtgca ttgtgtgtcg cctgcctcat gctctctata gaggaggatg 3259
 gtcactgtga cagcagcagc tcaagttagc atttcaagtg atttgggggt gcaatgataa 3319
 tgaagaatgg ccattttgta ccagggtctc gtattctgca acagcctgtt tgggaggctg 3379
 gagtggaaac aaaggggtgg catcaaagat gagaagccaa agcccctaca actccagcca 3439
 cccagccagg aggggtgtgc caatcacatt caggcatgcg aatgagctgg gccctgggtg 3499
 aggtgggggt ctggcctagt ggggaggggc ctggcctggg tggggcaggg cctggcctgg 3559
 tccaggcttg ggtccattc ccatcactgc tgtccctcct gaggtctgga ttggggatgg 3619
 ggacaaagaa atagcaagag atgagaaaca acagaaactt ttttctctaa aggactggtt 3679
 aaatcaattc tgatacagcc ttacaataca atagtatgca gtaaaaaaat aattgtatgt 3739
 ctttatatac taatatgtaa taatcttcag gtgaaaaagg caagccacag aaatgtgtat 3799
 agcgcacttc ccatttgtgt ttcagaaagg agtagaatat aaacacataa ttgcttatgt 3859
 atgcctattc agaataaatg ggtaacactg attacttttg ggaggggaac cagtaggttg 3919
 aggacaggag aggggaagggt ctaaacactt acacccttt gtacattttg aattttgaac 3979
 catgtgactg tattacctat tcaaaataaa caataaatgg gcccaaaaaa aaaaaaaaaa 4039
 a 4040

<210> 2

<211> 763

<212> PRT

<213> Homo sapiens

<400> 2

Met	Asn	Gln	Lys	Thr	Ile	Leu	Val	Leu	Leu	Ile	Leu	Ala	Val	Ile	Thr
1				5					10					15	
Ile	Phe	Ala	Leu	Val	Cys	Val	Leu	Leu	Val	Gly	Arg	Gly	Gly	Asp	Gly
		20						25					30		
Gly	Glu	Pro	Ser	Gln	Leu	Pro	His	Cys	Pro	Ser	Val	Ser	Pro	Ser	Ala
		35					40					45			
Gln	Pro	Trp	Thr	His	Pro	Gly	Gln	Ser	Gln	Leu	Phe	Ala	Asp	Leu	Ser
		50				55					60				
Arg	Glu	Glu	Leu	Thr	Ala	Val	Met	Arg	Phe	Leu	Thr	Gln	Arg	Leu	Gly
65					70					75				80	
Pro	Gly	Leu	Val	Asp	Ala	Ala	Gln	Ala	Arg	Pro	Ser	Asp	Asn	Cys	Val
				85					90					95	
Phe	Ser	Val	Glu	Leu	Gln	Leu	Pro	Pro	Lys	Ala	Ala	Ala	Leu	Ala	His
		100						105					110		
Leu	Asp	Arg	Gly	Ser	Pro	Pro	Pro	Ala	Arg	Glu	Ala	Leu	Ala	Ile	Val
		115					120					125			
Phe	Phe	Gly	Arg	Gln	Pro	Gln	Pro	Asn	Val	Ser	Glu	Leu	Val	Val	Gly
	130					135					140				
Pro	Leu	Pro	His	Pro	Ser	Tyr	Met	Arg	Asp	Val	Thr	Val	Glu	Arg	His
145					150					155				160	
Gly	Gly	Pro	Leu	Pro	Tyr	His	Arg	Arg	Pro	Val	Leu	Phe	Gln	Glu	Tyr
				165					170					175	

Leu Asp Ile Asp Gln Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser
 180 185 190
 Gly Leu Leu His His Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu
 195 200 205
 Val Thr Met Thr Thr Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala
 210 215 220
 Thr Trp Phe Gly Leu Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu
 225 230 235 240
 His His Val Gly Leu Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro
 245 250 255
 Ala Arg Trp Thr Ile Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp
 260 265 270
 Ser Leu Ala Gln Leu Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val
 275 280 285
 Val Leu Ile Pro Asp Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser
 290 295 300
 Pro Val Pro Pro Gly Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly
 305 310 315 320
 Pro Arg Phe Ser Val Gln Gly Ser Arg Val Ala Ser Ser Leu Trp Thr
 325 330 335
 Phe Ser Phe Gly Leu Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val
 340 345 350
 Arg Phe Gln Gly Glu Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala
 355 360 365
 Leu Ala Ile Tyr Gly Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr
 370 375 380
 Val Asp Gly Gly Phe Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg
 385 390 395 400
 Gly Val Asp Cys Pro Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu
 405 410 415
 Leu Glu Ser Gln Ala Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe
 420 425 430
 Glu Gln Asn Gln Gly Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr
 435 440 445
 Ser His Tyr Phe Gly Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser
 450 455 460
 Met Ser Thr Leu Leu Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His
 465 470 475 480
 Pro Ser Gly Ala Ile Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser
 485 490 495
 Ser Ala Phe Leu Phe Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser
 500 505 510
 Glu His Thr Leu Gly Thr Val His Thr His Ser Ala His Phe Lys Val
 515 520 525
 Asp Leu Asp Val Ala Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met
 530 535 540
 Val Phe Val Pro Met Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln
 545 550 555 560
 Arg Leu Gln Val Thr Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala
 565 570 575
 Phe Leu Val Gly Ser Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn
 580 585 590
 His Ser Asn Lys Trp Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu
 595 600 605
 Ser Phe Ala Gly Glu Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly
 610 615 620
 Phe Ser Trp Glu Arg Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu

180 185 190
 195 200 205
 210 215 220
 225 230 235 240
 245 250 255
 260 265 270
 275 280 285
 290 295 300
 305 310 315 320
 325 330 335
 340 345 350
 355 360 365
 370 375 380
 385 390 395 400
 405 410 415
 420 425 430
 435 440 445
 450 455 460
 465 470 475 480
 485 490 495
 500 505 510
 515 520 525
 530 535 540
 545 550 555 560
 565 570 575
 580 585 590
 595 600 605
 610 615 620

625		630		635		640
Glu Pro Ser Ser Ser Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro						
	645		650		655	
Thr Val Asp Phe Ser Asp Phe Ile Asn Asn Glu Thr Ile Ala Gly Lys						
	660		665		670	
Asp Leu Val Ala Trp Val Thr Ala Gly Phe Leu His Ile Pro His Ala						
	675		680		685	
Glu Asp Ile Pro Asn Thr Val Thr Val Gly Asn Gly Val Gly Phe Phe						
	690		695		700	
Leu Arg Pro Tyr Asn Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala						
	705		710		715	
Asp Ser Ile Tyr Phe Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val						
	725		730		735	
Asn Pro Leu Ala Cys Leu Pro Gln Ala Ala Ala Cys Ala Pro Asp Leu						
	740		745		750	
Pro Ala Phe Ser His Gly Gly Phe Ser His Asn						
	755		760			

<210> 3
 <211> 739
 <212> DNA
 <213> Schistosoma japonicum

<220>
 <221> CDS
 <222> (17) ... (670)

<400> 3	
tttaggtaac ttggtc atg tcc cct ata cta ggt tat tgg aaa att aag ggc	52
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly	
1 5 10	
ctt gtg caa ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat	100
Leu Val Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr	
15 20 25	
gaa gag cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa	148
Glu Glu His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys	
30 35 40	
aag ttt gaa ttg ggt ttg gag ttt ccc aat ctt cct tat tat att gat	196
Lys Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp	
45 50 55 60	
ggg gat gtt aaa tta aca cag tct atg gcc atc ata cgt tat ata gct	244
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala	
65 70 75	
gac aag cac aac atg ttg ggt ggt tgt cca aaa gag cgt gca gag att	292
Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile	
80 85 90	
tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt gtt tcg aga	340
Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg	
95 100 105	
att gca tat agt aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc	388

Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser
 110 115 120
 aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa 436
 Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys
 125 130 135 140
 aca tat tta aat ggt gat cat gta acc cat cct gac ttc atg ttg tat 484
 Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr
 145 150 155
 gac gct ctt gat gtt gtt tta tac atg gac cca atg tgc ctg gat gcg 532
 Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala
 160 165 170
 ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa 580
 Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln
 175 180 185
 att gat aag tac ttg aaa tcc agc aag tat ata gca tgg cct ttg cag 628
 Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln
 190 195 200
 ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct cca aaa 670
 Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys
 205 210 215
 taaattaaga atgattgttt tagtaaacat tattttatcac ttacaattaa actaaatata 730
 aatgtcgac 739
 <210> 4
 <211> 218
 <212> PRT
 <213> Schistosoma japonicum
 <400> 4
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu

110 115 120
 125 130 135 140
 145 150 155
 160 165 170
 175 180 185
 190 195 200
 205 210 215
 730
 739

				165					170					175			
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180					185					190				
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys								
	210					215											

<210> 5

<211> 218

<212> PRT

<213> Schistosoma japonicum

<400> 5

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro		
1				5				10						15			
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
			20					25					30				
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
		35				40					45						
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
	50				55					60							
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
65				70				75						80			
Met	Leu	Gly	Gly	Ser	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
			85					90						95			
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
		100						105					110				
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
	115					120						125					
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Ser	His	Lys	Thr	Tyr	Leu	Asn		
	130					135					140						
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
145			150					155						160			
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
		165						170					175				
Val	Ser	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
		180						185					190				
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
	195						200					205					
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys								
	210					215											

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Protease cleavage site

<400> 6

Glu	Ala	Leu	Phe	Gln	Gly												
1				5													

<210> 7

<211> 43

<212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 7
 ccggaattcc aacgcgtcca tgaaccagaa gacaatcctc gtg 43

<210> 8
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 8
 cccccaagct tgtcgactca ctagttgtga gagagaagcc ccccc 45

<210> 9
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 9
 gaggaagctt tgttccaagg tggagatggg ggtgaa 36

<210> 10
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 10
 gcattctagt tgtggtttgt c 21

<210> 11
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 11
 gccggaattc gacgcgtccc ctatactagg ttattgg 37

<210> 12
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
<223> PCR primer

<400> 12
ctctgcgcgc tcttttgag aaccaacat gttgtgc 37

<210> 13
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 13
ggttctccaa aagagcgcgc agagatttca atgcttgaag 40

<210> 14
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 14
atgagataaa cggctcttoga acattttcag catttc 36

<210> 15
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 15
gttcgaagac cgtttatctc ataaaacata tttaaattgt gatc 44

<210> 16
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 16
aaaagaaact agttttggga acgcatccag gca 33

<210> 17
<211> 40
<212> DNA
<213> Artificial Sequence

<220>

40

44

gac aag cac aac atg ttg ggt ggt tct cca aaa gag cgc gca gag att 384

Asp	Lys	His	Asn	Met	Leu	Gly	Gly	Ser	Pro	Lys	Glu	Arg	Ala	Glu	Ile	
		115					120					125				
tca	atg	ctt	gaa	gga	gcg	gtt	ttg	gat	att	aga	tac	ggg	gtt	tcg	aga	432
Ser	Met	Leu	Glu	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	
	130					135				140						
att	gca	tat	agt	aaa	gac	ttt	gaa	act	ctc	aaa	gtt	gat	ttt	ctt	agc	480
Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	
	145				150					155					160	
aag	cta	cct	gaa	atg	ctg	aaa	atg	ttc	gaa	gac	cgt	tta	tct	cat	aaa	528
Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Ser	His	Lys	
				165					170					175		
aca	tat	tta	aat	ggg	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	576
Thr	Tyr	Leu	Asn	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	
			180					185					190			
gac	gct	ctt	gat	gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	624
Asp	Ala	Leu	Asp	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	
		195					200					205				
ttc	cca	aaa	cta	gtt	tct	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	672
Phe	Pro	Lys	Leu	Val	Ser	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	
	210					215					220					
att	gat	aag	tac	ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	720
Ile	Asp	Lys	Tyr	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	
	225				230					235					240	
ggc	tgg	caa	gcc	acg	ttt	ggg	ggg	ggc	gac	cat	cct	cca	aag	tca	caa	768
Gly	Trp	Gln	Ala	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Gln	
				245					250					255		
agt	cag	gaa	gct	ttg	ttc	caa	ggg	gga	gat	ggg	ggg	gaa	ccc	agc	cag	816
Ser	Gln	Glu	Ala	Leu	Phe	Gln	Gly	Gly	Asp	Gly	Gly	Glu	Pro	Ser	Gln	
			260					265					270			
ctt	ccc	cat	tgc	ccc	tct	gta	tct	ccc	agt	gcc	cag	cct	tgg	aca	cac	864
Leu	Pro	His	Cys	Pro	Ser	Val	Ser	Pro	Ser	Ala	Gln	Pro	Trp	Thr	His	
		275					280					285				
cct	ggc	cag	agc	cag	ctg	ttt	gca	gac	ctg	agc	cga	gag	gag	ctg	acg	912
Pro	Gly	Gln	Ser	Gln	Leu	Phe	Ala	Asp	Leu	Ser	Arg	Glu	Glu	Leu	Thr	
	290					295					300					
gct	gtg	atg	cgc	ttt	ctg	acc	cag	cgg	ctg	ggg	cca	ggg	ctg	gtg	gat	960
Ala	Val	Met	Arg	Phe	Leu	Thr	Gln	Arg	Leu	Gly	Pro	Gly	Leu	Val	Asp	
	305				310					315					320	
gca	gcc	cag	gcc	cgg	ccc	tcg	gac	aac	tgt	gtc	ttc	tca	gtg	gag	ttg	1008
Ala	Ala	Gln	Ala	Arg	Pro	Ser	Asp	Asn	Cys	Val	Phe	Ser	Val	Glu	Leu	
				325				330						335		
cag	ctg	cct	ccc	aag	gct	gca	gcc	ctg	gct	cac	ttg	gac	agg	ggg	agc	1056
Gln	Leu	Pro	Pro	Lys	Ala	Ala	Ala	Leu	Ala	His	Leu	Asp	Arg	Gly	Ser	

115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335

340	345	350	
ccc cca cct gcc cgg gag gca ctg gcc atc gtc ttc ttt ggc agg caa			1104
Pro Pro Pro Ala Arg Glu Ala	Leu Ala Ile Val Phe Phe Gly Arg Gln		
355	360	365	
ccc cag ccc aac gtg agt gag ctg gtg gtg ggg cca ctg cct cac ccc			1152
Pro Gln Pro Asn Val Ser	Glu Leu Val Val Gly	Pro Leu Pro His Pro	
370	375	380	
tcc tac atg cgg gac gtg act gtg gag cgt cat gga ggc ccc ctg ccc			1200
Ser Tyr Met Arg Asp Val Thr Val Glu Arg His Gly Gly Pro Leu Pro			
385	390	395	400
tat cac cga cgc ccc gtg ctg ttc caa gag tac ctg gac ata gac cag			1248
Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr Leu Asp Ile Asp Gln			
405	410	415	
atg atc ttc aac aga gag ctg ccc cag gct tct ggg ctt ctc cac cac			1296
Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser Gly Leu Leu His His			
420	425	430	
tgt tgc ttc tac aag cac cgg gga cgg aac ctg gtg aca atg acc acg			1344
Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu Val Thr Met Thr Thr			
435	440	445	
gct ccc cgt ggt ctg caa tca ggg gac cgg gcc acc tgg ttt ggc ctc			1392
Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala Thr Trp Phe Gly Leu			
450	455	460	
tac tac aac atc tcg ggc gct ggg ttc ttc ctg cac cac gtg ggc ttg			1440
Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu His His Val Gly Leu			
465	470	475	480
gag ctg cta gtg aac cac aag gcc ctt gac cct gcc cgc tgg act atc			1488
Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro Ala Arg Trp Thr Ile			
485	490	495	
cag aag gtg ttc tat caa ggc cgc tac tac gac agc ctg gcc cag ctg			1536
Gln Lys Val Phe Tyr Gln Gly Arg Tyr Asp Ser Leu Ala Gln Leu			
500	505	510	
gag gcc cag ttt gag gcc ggc ctg gtg aat gtg gtg ctg atc cca gac			1584
Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val Val Leu Ile Pro Asp			
515	520	525	
aat ggc aca ggt ggg tcc tgg tcc ctg aag tcc cct gtg ccc ccg ggt			1632
Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser Pro Val Pro Pro Gly			
530	535	540	
cca gct ccc cct cta cag ttc tat ccc caa ggc ccc cgc ttc agt gtc			1680
Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly Pro Arg Phe Ser Val			
545	550	555	560
cag gga agt cga gtg gcc tcc tca ctg tgg act ttc tcc ttt ggc ctc			1728
Gln Gly Ser Arg Val Ala Ser Ser Leu Trp Thr Phe Ser Phe Gly Leu			
565	570	575	

1104
1152
1200
1248
1296
1344
1392
1440
1488
1536
1584
1632
1680
1728

gga gca ttc agt ggc cca agg atc ttt gac gtt cgc ttc caa gga gaa	1776
Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val Arg Phe Gln Gly Glu	
580 585 590	
aga cta gtt tat gag ata agc ctc caa gag gcc ttg gcc atc tat ggt	1824
Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala Leu Ala Ile Tyr Gly	
595 600 605	
gga aat tcc cca gca gca atg acg acc cgc tat gtg gat gga ggc ttt	1872
Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr Val Asp Gly Gly Phe	
610 615 620	
ggc atg ggc aag tac acc acg ccc ctg acc cgt ggg gtg gac tgc ccc	1920
Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg Gly Val Asp Cys Pro	
625 630 635 640	
tac ttg gcc acc tac gtg gac tgg cac ttc ctt ttg gag tcc cag gcc	1968
Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu Leu Glu Ser Gln Ala	
645 650 655	
ccc aag aca ata cgt gat gcc ttt tgt gtg ttt gaa cag aac cag ggc	2016
Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe Glu Gln Asn Gln Gly	
660 665 670	
ctc ccc ctg cgg cga cac cac tca gat ctc tac tcg cac tac ttt ggg	2064
Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly	
675 680 685	
ggt ctt gcg gaa acg gtg ctg gtc gtc aga tct atg tcc acc ttg ctc	2112
Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser Met Ser Thr Leu Leu	
690 695 700	
aac tat gac tat gtg tgg gat acg gtc ttc cac ccc agt ggg gcc ata	2160
Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile	
705 710 715 720	
gaa ata cga ttc tat gcc acg ggc tac atc agc tcg gca ttc ctc ttt	2208
Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe	
725 730 735	
ggt gct act ggg aag tac ggg aac caa gtg tca gag cac acc ctg ggc	2256
Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly	
740 745 750	
acg gtc cac acc cac agc gcc cac ttc aag gtg gat ctg gat gta gca	2304
Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala	
755 760 765	
gga ctg gag aac tgg gtc tgg gcc gag gat atg gtc ttt gtc ccc atg	2352
Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met	
770 775 780	
gct gtg ccc tgg agc cct gag cac cag ctg cag agg ctg cag gtg acc	2400
Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr	
785 790 795 800	

cgg aag ctg ctg gag atg gag gag cag gcc gcc ttc ctc gtg gga agc Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser 805 810 815	2448
gcc acc cct cgc tac ctg tac ctg gcc agc aac cac agc aac aag tgg Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp 820 825 830	2496
ggt cac ccc cgg ggc tac cgc atc cag atg ctc agc ttt gct gga gag Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu 835 840 845	2544
ccg ctg ccc caa aac agc tcc atg gcg aga ggc ttc agc tgg gag agg Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg 850 855 860	2592
tac cag ctg gct gtg acc cag cgg aag gag gag gag ccc agt agc agc Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser 865 870 875 880	2640
agc gtt ttc aat cag aat gac cct tgg gcc ccc act gtg gat ttc agt Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro Thr Val Asp Phe Ser 885 890 895	2688
gac ttc atc aac aat gag acc att gct gga aag gat ttg gtg gcc tgg Asp Phe Ile Asn Asn Glu Thr Ile Ala Gly Lys Asp Leu Val Ala Trp 900 905 910	2736
gtg aca gct ggt ttt ctg cat atc cca cat gca gag gac att cct aac Val Thr Ala Gly Phe Leu His Ile Pro His Ala Glu Asp Ile Pro Asn 915 920 925	2784
aca gtg act gtg ggg aac ggc gtg ggc ttc ttc ctc cga ccc tat aac Thr Val Thr Val Gly Asn Gly Val Gly Phe Phe Leu Arg Pro Tyr Asn 930 935 940	2832
ttc ttt gac gaa gac ccc tcc ttc tac tct gcc gac tcc atc tac ttc Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala Asp Ser Ile Tyr Phe 945 950 955 960	2880
cga ggg gac cag gat gct ggg gcc tgc gag gtc aac ccc cta gct tgc Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val Asn Pro Leu Ala Cys 965 970 975	2928
ctg ccc cag gct gct gcc tgt gcc ccc gac ctc cct gcc ttc tcc cac Leu Pro Gln Ala Ala Ala Cys Ala Pro Asp Leu Pro Ala Phe Ser His 980 985 990	2976
ggg ggc ttc tct cac aac tagtgagtcg ac Gly Gly Phe Ser His Asn 995	3006

<210> 20

<211> 998

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant construct

<400> 20

Met	Asp	Trp	Leu	Arg	Asn	Leu	Leu	Phe	Leu	Met	Ala	Ala	Ala	Gln	Ser	1	5	10	15
Ile	Asn	Ala	Ala	Gln	His	Asp	Glu	Ala	Val	Asp	Asn	Lys	Phe	Asn	Lys	20	25	30	
Glu	Gln	Gln	Asn	Ala	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	35	40	45	
Leu	Val	Gln	Pro	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	50	55	60	
Glu	Glu	His	Leu	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	65	70	75	80
Lys	Phe	Glu	Leu	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	85	90	95	
Gly	Asp	Val	Lys	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	100	105	110	
Asp	Lys	His	Asn	Met	Leu	Gly	Gly	Ser	Pro	Lys	Glu	Arg	Ala	Glu	Ile	115	120	125	
Ser	Met	Leu	Glu	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	130	135	140	
Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	145	150	155	160
Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Ser	His	Lys	165	170	175	
Thr	Tyr	Leu	Asn	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	180	185	190	
Asp	Ala	Leu	Asp	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	195	200	205	
Phe	Pro	Lys	Leu	Val	Ser	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	210	215	220	
Ile	Asp	Lys	Tyr	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	225	230	235	240
Gly	Trp	Gln	Ala	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Gln	245	250	255	
Ser	Gln	Glu	Ala	Leu	Phe	Gln	Gly	Gly	Asp	Gly	Gly	Glu	Pro	Ser	Gln	260	265	270	
Leu	Pro	His	Cys	Pro	Ser	Val	Ser	Pro	Ser	Ala	Gln	Pro	Trp	Thr	His	275	280	285	
Pro	Gly	Gln	Ser	Gln	Leu	Phe	Ala	Asp	Leu	Ser	Arg	Glu	Glu	Leu	Thr	290	295	300	
Ala	Val	Met	Arg	Phe	Leu	Thr	Gln	Arg	Leu	Gly	Pro	Gly	Leu	Val	Asp	305	310	315	320
Ala	Ala	Gln	Ala	Arg	Pro	Ser	Asp	Asn	Cys	Val	Phe	Ser	Val	Glu	Leu	325	330	335	
Gln	Leu	Pro	Pro	Lys	Ala	Ala	Ala	Leu	Ala	His	Leu	Asp	Arg	Gly	Ser	340	345	350	
Pro	Pro	Pro	Ala	Arg	Glu	Ala	Leu	Ala	Ile	Val	Phe	Phe	Gly	Arg	Gln	355	360	365	
Pro	Gln	Pro	Asn	Val	Ser	Glu	Leu	Val	Val	Gly	Pro	Leu	Pro	His	Pro	370	375	380	
Ser	Tyr	Met	Arg	Asp	Val	Thr	Val	Glu	Arg	His	Gly	Gly	Pro	Leu	Pro	385	390	395	400
Tyr	His	Arg	Arg	Pro	Val	Leu	Phe	Gln	Glu	Tyr	Leu	Asp	Ile	Asp	Gln	405	410	415	

Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser Gly Leu Leu His His
 420 425 430
 Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu Val Thr Met Thr Thr
 435 440 445
 Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala Thr Trp Phe Gly Leu
 450 455 460
 Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu His His Val Gly Leu
 465 470 475 480
 Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro Ala Arg Trp Thr Ile
 485 490 495
 Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp Ser Leu Ala Gln Leu
 500 505 510
 Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val Val Leu Ile Pro Asp
 515 520 525
 Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser Pro Val Pro Pro Gly
 530 535 540
 Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly Pro Arg Phe Ser Val
 545 550 555 560
 Gln Gly Ser Arg Val Ala Ser Ser Leu Trp Thr Phe Ser Phe Gly Leu
 565 570 575
 Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val Arg Phe Gln Gly Glu
 580 585 590
 Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala Leu Ala Ile Tyr Gly
 595 600 605
 Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr Val Asp Gly Gly Phe
 610 615 620
 Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg Gly Val Asp Cys Pro
 625 630 635 640
 Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu Leu Glu Ser Gln Ala
 645 650 655
 Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe Glu Gln Asn Gln Gly
 660 665 670
 Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly
 675 680 685
 Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser Met Ser Thr Leu Leu
 690 695 700
 Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile
 705 710 715 720
 Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe
 725 730 735
 Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly
 740 745 750
 Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala
 755 760 765
 Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met
 770 775 780
 Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr
 785 790 795 800
 Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser
 805 810 815
 Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp
 820 825 830
 Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu
 835 840 845
 Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg
 850 855 860
 Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser

[illegible]